

aga gtt ata agc aat aaa gta gaa aaa gac agc gat agt gaa caa agg 245
Arg Val Ile Ser Asn Lys Val Glu Lys Asp Ser Asp Ser Glu Gln Arg

60						65						70						
gga	aga	aag	aag	gaa	aca	act	ggg	ccc	aat	aac	tat	cat	aat	tta	gaa	293		
Gly	Arg	Lys	Lys	Glu	Thr	Thr	Gly	Pro	Asn	Asn	Tyr	His	Asn	Leu	Glu			
		75					80					85						
gag	aag	caa	gcg	agt	gcc	att	tct	ctt	gac	gct	gat	gat	gaa	gat	ctc	341		
Glu	Lys	Gln	Ala	Ser	Ala	Ile	Ser	Leu	Asp	Ala	Asp	Asp	Glu	Asp	Leu			
	90					95					100							
gat	gaa	att	att	tct	tat	tcg	cat	gac	ggg	aac	tat	gac	agc	tct	cat	389		
Asp	Glu	Ile	Ile	Ser	Tyr	Ser	His	Asp	Gly	Asn	Tyr	Asp	Ser	Ser	His			
105					110					115					120			
aaa	act	ttc	tcc	ttt	tcc	tta	cca	ttt	ggt	aat	aca	aat	ttc	cga	tca	437		
Lys	Thr	Phe	Ser	Phe	Ser	Leu	Pro	Phe	Gly	Asn	Thr	Asn	Phe	Arg	Ser			
				125					130					135				
agt	tca	cca	tta	gcc	ata	att	aaa	act	gtg	ctt	ccc	aag	act	cca	gat	485		
Ser	Ser	Pro	Leu	Ala	Ile	Ile	Lys	Thr	Val	Leu	Pro	Lys	Thr	Pro	Asp			
			140					145					150					
gag	ttc	atc	aaa	aag	aat	cta	aga	aag	aat	gag	atc	aag	caa	aaa	ctg	533		
Glu	Phe	Ile	Lys	Lys	Asn	Leu	Arg	Lys	Asn	Glu	Ile	Lys	Gln	Lys	Leu			
		155					160					165						
aaa	aaa	tca	acc	tcc	att	tct	tcc	ttg	gaa	gag	ata	gaa	tta	ttt	aaa	581		
Lys	Lys	Ser	Thr	Ser	Ile	Ser	Ser	Leu	Glu	Glu	Ile	Glu	Leu	Phe	Lys			
	170					175					180							
tac	gaa	agg	ggc	att	gat	aat	tca	agg	tta	agg	gct	gtt	aaa	gaa	tct	629		
Tyr	Glu	Arg	Gly	Ile	Asp	Asn	Ser	Arg	Leu	Arg	Ala	Val	Lys	Glu	Ser			
185					190					195					200			
ttg	gaa	atg	gat	gcc	ttg	aag	aac	tcc	att	aag	caa	ata	aca	gca	gac	677		
Leu	Glu	Met	Asp	Ala	Leu	Lys	Asn	Ser	Ile	Lys	Gln	Ile	Thr	Ala	Asp			
				205					210					215				
cca	ttc	gac	aaa	act	cat	gac	gga	tat	tac	cgt	tcg	cgt	tta	gaa	tct	725		
Pro	Phe	Asp	Lys	Thr	His	Asp	Gly	Tyr	Tyr	Arg	Ser	Arg	Leu	Glu	Ser			
			220					225					230					
ata	tgg	aat	gaa	ttg	gaa	gga	gat	gtc	gtt	ata	atg	ggt	gga	tat	cga	773		
Ile	Trp	Asn	Glu	Leu	Glu	Gly	Asp	Val	Val	Ile	Met	Gly	Gly	Tyr	Arg			
		235					240					245						
ggt	agt	gtg	cta	agg	gat	gct	act	act	cat	aag	cga	att	tgg	atc	cca	821		
Gly	Ser	Val	Leu	Arg	Asp	Ala	Thr	Thr	His	Lys	Arg	Ile	Trp	Ile	Pro			
	250					255					260							
tta	aag	gca	ggt	ttg	aat	atg	acg	aaa	gtc	gat	tta	ttg	atc	gga	cct	869		
Leu	Lys	Ala	Gly	Leu	Asn	Met	Thr	Lys	Val	Asp	Leu	Leu	Ile	Gly	Pro			
265					270					275					280			
aat	gac	gaa	gat	gaa	ctt	aaa	act	cag	aag	gag	att	gtc	cct	gat	gga	917		
Asn	Asp	Glu	Asp	Glu	Leu	Lys	Thr	Gln	Lys	Glu	Ile	Val	Pro	Asp	Gly			
				285					290					295				

atg cta aca cat ata ggg cct gtt gat atc tct aag agg ttg ata aag	965
Met Leu Thr His Ile Gly Pro Val Asp Ile Ser Lys Arg Leu Ile Lys	
300 305 310	
agg cta gac gca aat cct aat tta aat gtt cag cag ttt ggc tat gat	1013
Arg Leu Asp Ala Asn Pro Asn Leu Asn Val Gln Gln Phe Gly Tyr Asp	
315 320 325	
tgg aga tta tcc ttg gac ata tct gcc aag cat tta acg act aaa cta	1061
Trp Arg Leu Ser Leu Asp Ile Ser Ala Lys His Leu Thr Thr Lys Leu	
330 335 340	
gag gaa att tac aat aag caa aaa aat aag aag gga ata tac atc att	1109
Glu Glu Ile Tyr Asn Lys Gln Lys Asn Lys Lys Gly Ile Tyr Ile Ile	
345 350 355 360	
gcc cat tca atg ggc gga ttg gtc gca cat aaa gtg ttg caa gac tgt	1157
Ala His Ser Met Gly Gly Leu Val Ala His Lys Val Leu Gln Asp Cys	
365 370 375	
act cat ttg ata aga ggt att att tac gtg ggt tcc cca agc caa tgt	1205
Thr His Leu Ile Arg Gly Ile Ile Tyr Val Gly Ser Pro Ser Gln Cys	
380 385 390	
cca aat att tta ggt cct att agg ttt gga gat gat gtg atg tgg aat	1253
Pro Asn Ile Leu Gly Pro Ile Arg Phe Gly Asp Asp Val Met Trp Asn	
395 400 405	
aaa cta ttt tca cta aga acc aac ttt ttt atg aga agt agt ttc tat	1301
Lys Leu Phe Ser Leu Arg Thr Asn Phe Phe Met Arg Ser Ser Phe Tyr	
410 415 420	
ttt cta ccg tta gat ggt aga tgt ttt gtt gac aaa att acc tta gag	1349
Phe Leu Pro Leu Asp Gly Arg Cys Phe Val Asp Lys Ile Thr Leu Glu	
425 430 435 440	
agg tat gat ttc gat ttt ttt gat aca gat gtt tgg aaa acc ctt ggc	1397
Arg Tyr Asp Phe Asp Phe Phe Asp Thr Asp Val Trp Lys Thr Leu Gly	
445 450 455	
ttg tca cct ctc gtc aat gag aaa aga gag gaa tca gct cac gaa aaa	1445
Leu Ser Pro Leu Val Asn Glu Lys Arg Glu Glu Ser Ala His Glu Lys	
460 465 470	
tca aaa tta tta cca agg aaa acg aaa tca gcg ctt tcg ctt aaa gct	1493
Ser Lys Leu Leu Pro Arg Lys Thr Lys Ser Ala Leu Ser Leu Lys Ala	
475 480 485	
acc cta aac gca act acc aag ttt gtc cta aat gca cct gtt gtt agg	1541
Thr Leu Asn Ala Thr Thr Lys Phe Val Leu Asn Ala Pro Val Val Arg	
490 495 500	
aat gta gcc ggc aat aat aaa cag gta cca agg gat gtg cct ttc gat	1589
Asn Val Ala Gly Asn Asn Lys Gln Val Pro Arg Asp Val Pro Phe Asp	
505 510 515 520	

gaa gtc ttc cat aca tct tat gaa gat agc tgt gaa tat tta gcg aga 1637
 Glu Val Phe His Thr Ser Tyr Glu Asp Ser Cys Glu Tyr Leu Ala Arg
 525 530 535

act tta aaa cgt aca aag aat tat ttg gat agc tta gat tac gac ccg 1685
 Thr Leu Lys Arg Thr Lys Asn Tyr Leu Asp Ser Leu Asp Tyr Asp Pro
 540 545 550

aac aaa gaa tat cct cca ttg gcc atg gtt tac ggt aac aag gtt ccc 1733
 Asn Lys Glu Tyr Pro Pro Leu Ala Met Val Tyr Gly Asn Lys Val Pro
 555 560 565

act gtt aga ggt gct aaa gtg aac ggt ata caa gat ata aaa gat ggg 1781
 Thr Val Arg Gly Ala Lys Val Asn Gly Ile Gln Asp Ile Lys Asp Gly
 570 575 580

aat tat gaa gat ttt tac tat ggt ccg ggc gac ggt gtt gtt cac cat 1829
 Asn Tyr Glu Asp Phe Tyr Tyr Gly Pro Gly Asp Gly Val Val His His
 585 590 595 600

aaa tgg tta ttg cct gaa cag aga ggc ttt cca gtt gtt tgt aaa atc 1877
 Lys Trp Leu Leu Pro Glu Gln Arg Gly Phe Pro Val Val Cys Lys Ile
 605 610 615

gcc agt tct tca ggt cat gtt agc tta atg acg gat ttg aaa tca atg 1925
 Ala Ser Ser Ser Gly His Val Ser Leu Met Thr Asp Leu Lys Ser Met
 620 625 630

gca aaa gca ttc ata tct atc gtc gac agc gaa aaa gaa gga aga aga 1973
 Ala Lys Ala Phe Ile Ser Ile Val Asp Ser Glu Lys Glu Gly Arg Arg
 635 640 645

tct cga aca cga act tct tca tgaaaggctt tttattcctt tgtttactat 2024
 Ser Arg Thr Arg Thr Ser Ser
 650 655

tcatatctgc atttttcttt ttaccaaagt tccgcatgtc aaaaaaatc tggcaacgca 2084

ccgcgaataa aaataaataa ttttttttta tcttttagttg cctaaatact atttatttcg 2144

tcaattttac aacctctttt atatacacca ttogatttcc cacgaagtaa aataataatt 2204

ctataaacag atttatctga tatgtctaat ttccctctcc attttcatta ttgtccttct 2264

tgctcttctc cgatgtcaaa attaaccttc agccataagc tgcattgcgt acattggggt 2324

aataattgat aaccagaatg actccgttcc atagcgtcta cattatcaat gcattcatct 2384

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<210> 2

<211> 655

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

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Asn	Lys	Gln	Cys	Leu	Ser	Asp	Ser	Ser	Asp	Ser	Gly	Ser	Asp	Val	Ser	20	25	30	
Phe	Phe	Ser	Val	Asn	Glu	Ser	Glu	Gly	Glu	Leu	Asp	Thr	Met	Glu	Lys	35	40	45	
Val	Asp	Thr	Leu	Ile	Gly	Gly	Ala	Arg	Val	Ile	Ser	Asn	Lys	Val	Glu	50	55	60	
Lys	Asp	Ser	Asp	Ser	Glu	Gln	Arg	Gly	Arg	Lys	Lys	Glu	Thr	Thr	Gly	65	70	75	80
Pro	Asn	Asn	Tyr	His	Asn	Leu	Glu	Glu	Lys	Gln	Ala	Ser	Ala	Ile	Ser	85	90	95	
Leu	Asp	Ala	Asp	Asp	Glu	Asp	Leu	Asp	Glu	Ile	Ile	Ser	Tyr	Ser	His	100	105	110	
Asp	Gly	Asn	Tyr	Asp	Ser	Ser	His	Lys	Thr	Phe	Ser	Phe	Ser	Leu	Pro	115	120	125	
Phe	Gly	Asn	Thr	Asn	Phe	Arg	Ser	Ser	Ser	Pro	Leu	Ala	Ile	Ile	Lys	130	135	140	
Thr	Val	Leu	Pro	Lys	Thr	Pro	Asp	Glu	Phe	Ile	Lys	Lys	Asn	Leu	Arg	145	150	155	160
Lys	Asn	Glu	Ile	Lys	Gln	Lys	Leu	Lys	Lys	Ser	Thr	Ser	Ile	Ser	Ser	165	170	175	
Leu	Glu	Glu	Ile	Glu	Leu	Phe	Lys	Tyr	Glu	Arg	Gly	Ile	Asp	Asn	Ser	180	185	190	
Arg	Leu	Arg	Ala	Val	Lys	Glu	Ser	Leu	Glu	Met	Asp	Ala	Leu	Lys	Asn	195	200	205	
Ser	Ile	Lys	Gln	Ile	Thr	Ala	Asp	Pro	Phe	Asp	Lys	Thr	His	Asp	Gly	210	215	220	
Tyr	Tyr	Arg	Ser	Arg	Leu	Glu	Ser	Ile	Trp	Asn	Glu	Leu	Glu	Gly	Asp	225	230	235	240
Val	Val	Ile	Met	Gly	Gly	Tyr	Arg	Gly	Ser	Val	Leu	Arg	Asp	Ala	Thr	245	250	255	
Thr	His	Lys	Arg	Ile	Trp	Ile	Pro	Leu	Lys	Ala	Gly	Leu	Asn	Met	Thr	260	265	270	
Lys	Val	Asp	Leu	Leu	Ile	Gly	Pro	Asn	Asp	Glu	Asp	Glu	Leu	Lys	Thr	275	280	285	
Gln	Lys	Glu	Ile	Val	Pro	Asp	Gly	Met	Leu	Thr	His	Ile	Gly	Pro	Val	290	295	300	

Asp Ile Ser Lys Arg Leu Ile Lys Arg Leu Asp Ala Asn Pro Asn Leu
 305 310 315 320
 Asn Val Gln Gln Phe Gly Tyr Asp Trp Arg Leu Ser Leu Asp Ile Ser
 325 330 335
 Ala Lys His Leu Thr Thr Lys Leu Glu Glu Ile Tyr Asn Lys Gln Lys
 340 345 350
 Asn Lys Lys Gly Ile Tyr Ile Ile Ala His Ser Met Gly Gly Leu Val
 355 360 365
 Ala His Lys Val Leu Gln Asp Cys Thr His Leu Ile Arg Gly Ile Ile
 370 375 380
 Tyr Val Gly Ser Pro Ser Gln Cys Pro Asn Ile Leu Gly Pro Ile Arg
 385 390 395 400
 Phe Gly Asp Asp Val Met Trp Asn Lys Leu Phe Ser Leu Arg Thr Asn
 405 410 415
 Phe Phe Met Arg Ser Ser Phe Tyr Phe Leu Pro Leu Asp Gly Arg Cys
 420 425 430
 Phe Val Asp Lys Ile Thr Leu Glu Arg Tyr Asp Phe Asp Phe Phe Asp
 435 440 445
 Thr Asp Val Trp Lys Thr Leu Gly Leu Ser Pro Leu Val Asn Glu Lys
 450 455 460
 Arg Glu Glu Ser Ala His Glu Lys Ser Lys Leu Leu Pro Arg Lys Thr
 465 470 475 480
 Lys Ser Ala Leu Ser Leu Lys Ala Thr Leu Asn Ala Thr Thr Lys Phe
 485 490 495
 Val Leu Asn Ala Pro Val Val Arg Asn Val Ala Gly Asn Asn Lys Gln
 500 505 510
 Val Pro Arg Asp Val Pro Phe Asp Glu Val Phe His Thr Ser Tyr Glu
 515 520 525
 Asp Ser Cys Glu Tyr Leu Ala Arg Thr Leu Lys Arg Thr Lys Asn Tyr
 530 535 540
 Leu Asp Ser Leu Asp Tyr Asp Pro Asn Lys Glu Tyr Pro Pro Leu Ala
 545 550 555 560
 Met Val Tyr Gly Asn Lys Val Pro Thr Val Arg Gly Ala Lys Val Asn
 565 570 575
 Gly Ile Gln Asp Ile Lys Asp Gly Asn Tyr Glu Asp Phe Tyr Tyr Gly
 580 585 590
 Pro Gly Asp Gly Val Val His His Lys Trp Leu Leu Pro Glu Gln Arg
 595 600 605

Gly	Phe	Pro	Val	Val	Cys	Lys	Ile	Ala	Ser	Ser	Ser	Gly	His	Val	Ser
610						615					620				
Leu	Met	Thr	Asp	Leu	Lys	Ser	Met	Ala	Lys	Ala	Phe	Ile	Ser	Ile	Val
625					630					635					640
Asp	Ser	Glu	Lys	Glu	Gly	Arg	Arg	Ser	Arg	Thr	Arg	Thr	Ser	Ser	
				645					650					655	